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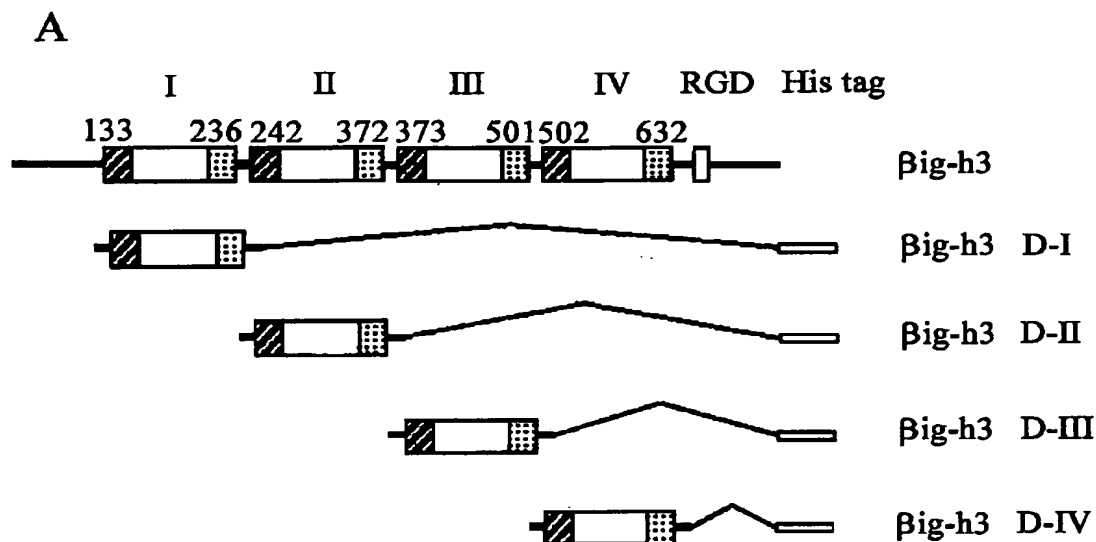
FIG. 1

BIGH3_HUMAN	161	SNVNI	EL	LN	NA	RY	HM	VGRR	VT	DEL	KH	GMT	190
BIGH3-PIG	161	SNVNI	EL	LN	NA	RY	HM	VDRR	VT	DEL	KH	GMA	190
BIGH3_CHICK	154	SNVNI	EL	LN	NA	RY	HM	VNKR	VT	DD	LKH	GTT	183
OSF2_MOUSE	157	NNVN	VE	LN	NA	RY	HM	VNKR	MT	TK	DLKH	GMV	186
BIGH3_HUMAN	298	-GDPE	AR	DL	LN	NH	II	KSAM	CAEA	IV	AGLS	326	
BIGH3-PIG	298	-GDPE	AR	DL	LN	NH	II	KSAM	CAEA	IV	AGLS	326	
BIGH3_CHICK	290	-GDPE	AR	DL	LN	NH	II	KSAM	CAEA	IV	AGLT	318	
OSF2_HUMAN	292	-GDKV	ASEA	DM	KY	HM	II	NT	LQ	CE	SI	MG	320
OSF2_MOUSE	294	-GDKV	ASEA	DM	KY	HM	II	NT	LQ	CE	SI	MG	322
BIGH3_HUMAN	560	-GDARE	LAN	IL	KY	HM	II	GD	EL	IV	SG	GIG	588
BIGH3-PIG	560	-GNAKE	LAN	IL	KY	HM	II	VG	DE	IV	SG	GIG	588
BIGH3_CHICK	552	-GNAKE	LAN	IL	KY	HM	II	MA	DE	IV	SG	AV	580
SLL1735 homolog	59	-QNPP	Q	LA	FI	LT	YH	VA	AG	FI	TK	DD	87
SLL1735	59	-QNIP	Q	LA	FI	LT	YH	VV	AG	KFT	QA	LL	87
SLL1483	104	PENK	DF	LV	FI	LT	YH	VV	PG	RI	TAA	QV	132
OSF2_HUMAN	554	-RDKNA	LQ	NI	IL	YH	II	TP	GV	FI	IG	KGF	582
OSF2_MOUSE	556	-GDKNA	LQ	NI	IL	YH	II	TP	GV	FI	IG	KGF	584
MP83 MYCTU	164	-TDAR	KL	SS	II	TY	HM	VI	AG	Q--	AS	PS	190
MPT83	145	-TDAR	KL	SS	II	TY	HM	VI	AG	Q--	AS	PS	171
Q48948_MYCBO	119	-TNSS	ML	TS	II	TY	HM	VV	AG	Q--	TSP	AN	145
Q50769_MYCTU	119	-TNSS	ML	TS	II	TY	HM	VV	AG	Q--	TSP	AN	145
Putative Secreted protein	132	-NDRA	Q	PK	VT	YH	II	VV	EH	KRI	TKA	Q	160
Fasciclin	485	EG-RGC	AS	NI	LK	NH	II	LD	LT	FC	SI	AT	513
HLC-32	284	KDPAG	K	ERN	LL	KY	HM	VI	SD	VK	YS	VS	313
Fasciclin	775	-SKPA	DP	MA	LV	KT	TH	II	VE	DV	VCC	AG	803
BIGH3_HUMAN	432	RNLL	R	NH	II	KD	Q	LA	SK	YI	YH	GQ	464
BIGH3-PIG	432	KNLL	L	NH	II	KD	Q	LA	SK	YI	YH	GQ	464
BIGH3_CHICK	424	KNLL	L	NH	II	KD	Q	LA	SK	YI	YH	GQ	456
OSF2_HUMAN	426	-KLII	Q	NH	II	KV	KV	GL	NI	YH	YN	GQ	458
OSF2_MOUSE	428	-KLII	Q	NH	II	KV	KV	GL	NI	YH	YN	GQ	460

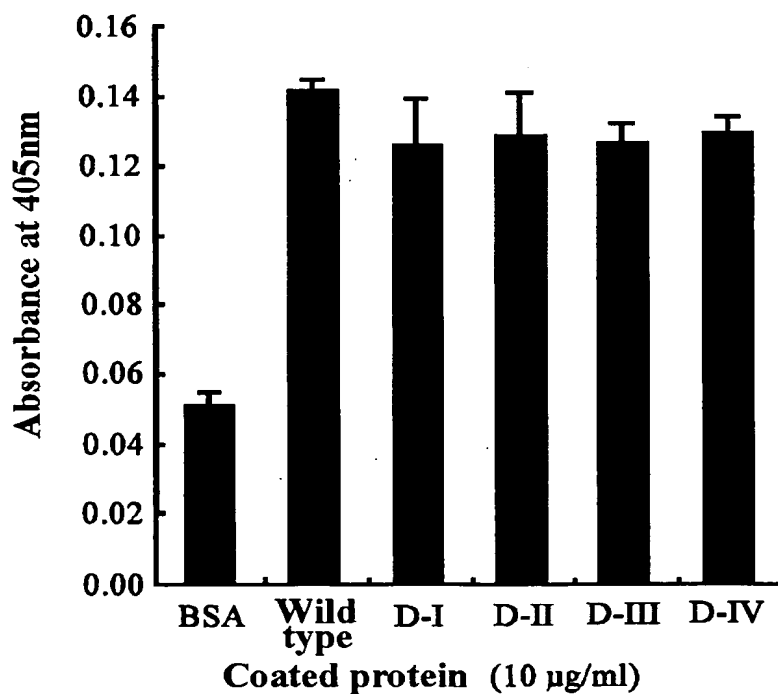
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FIG. 2

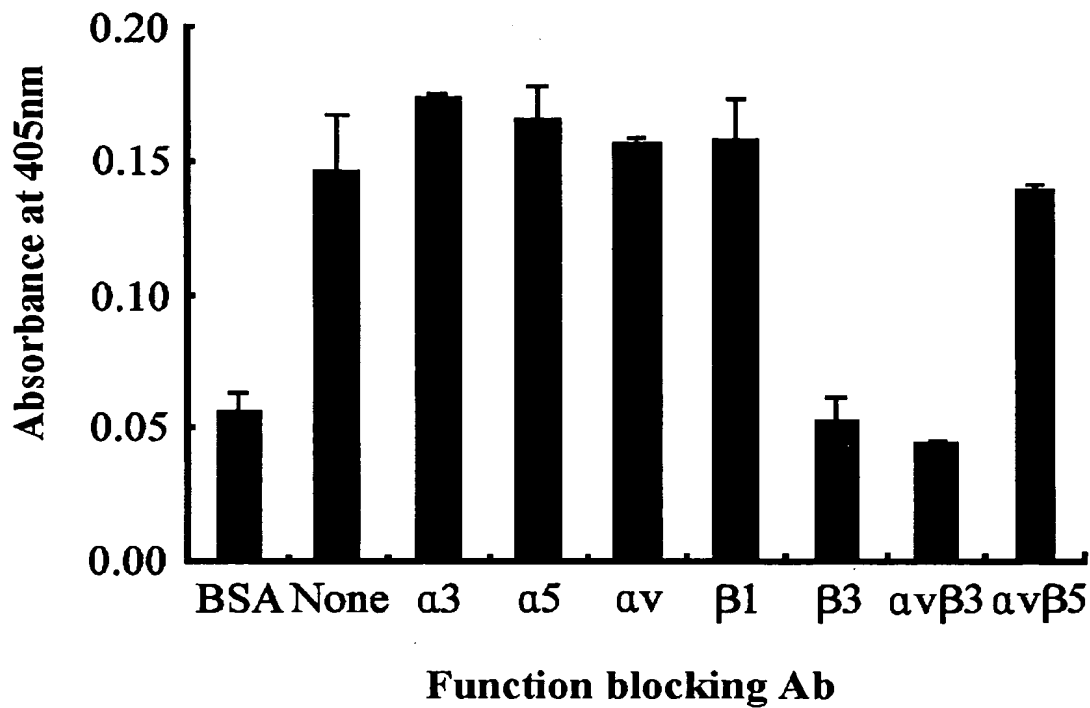


B



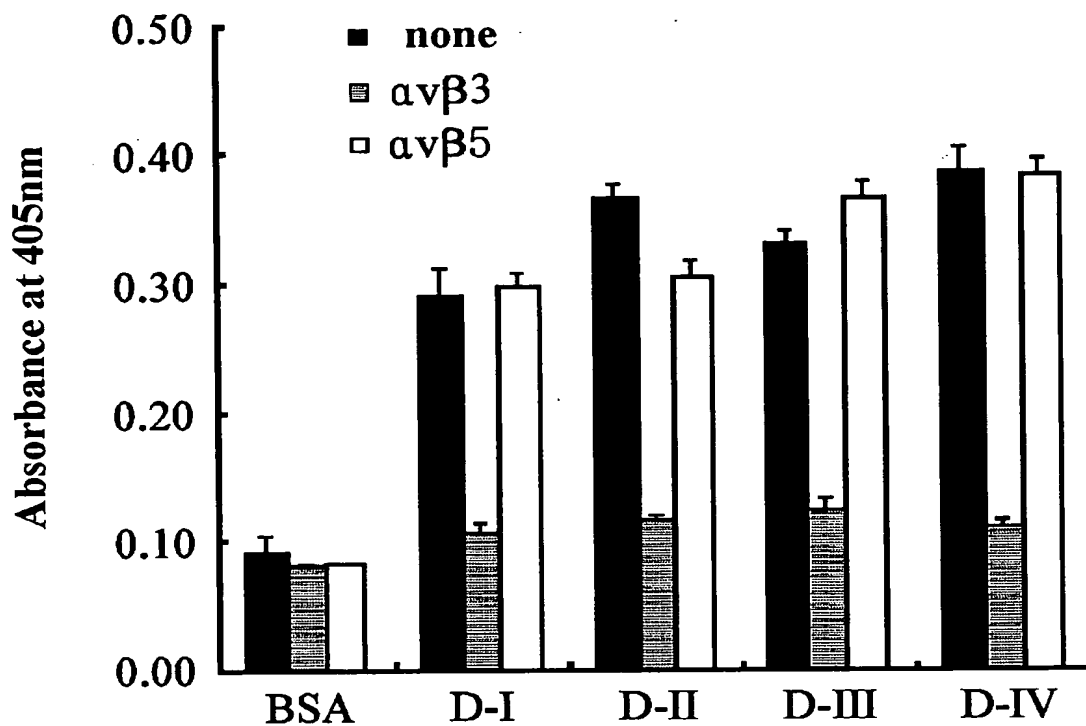
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FIG. 3a



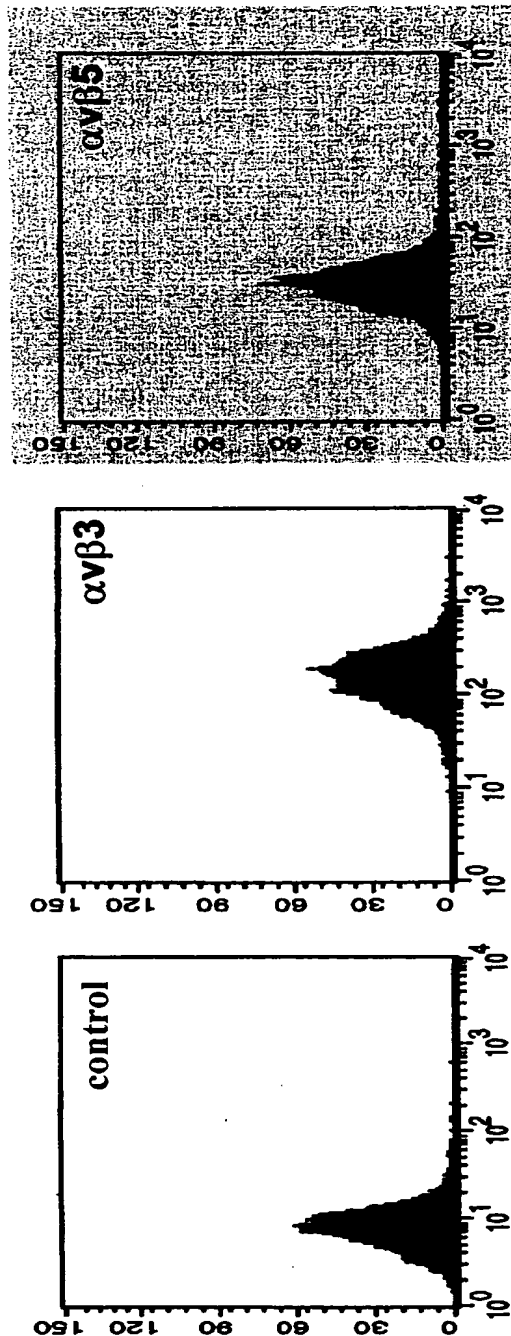
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FIG. 3b



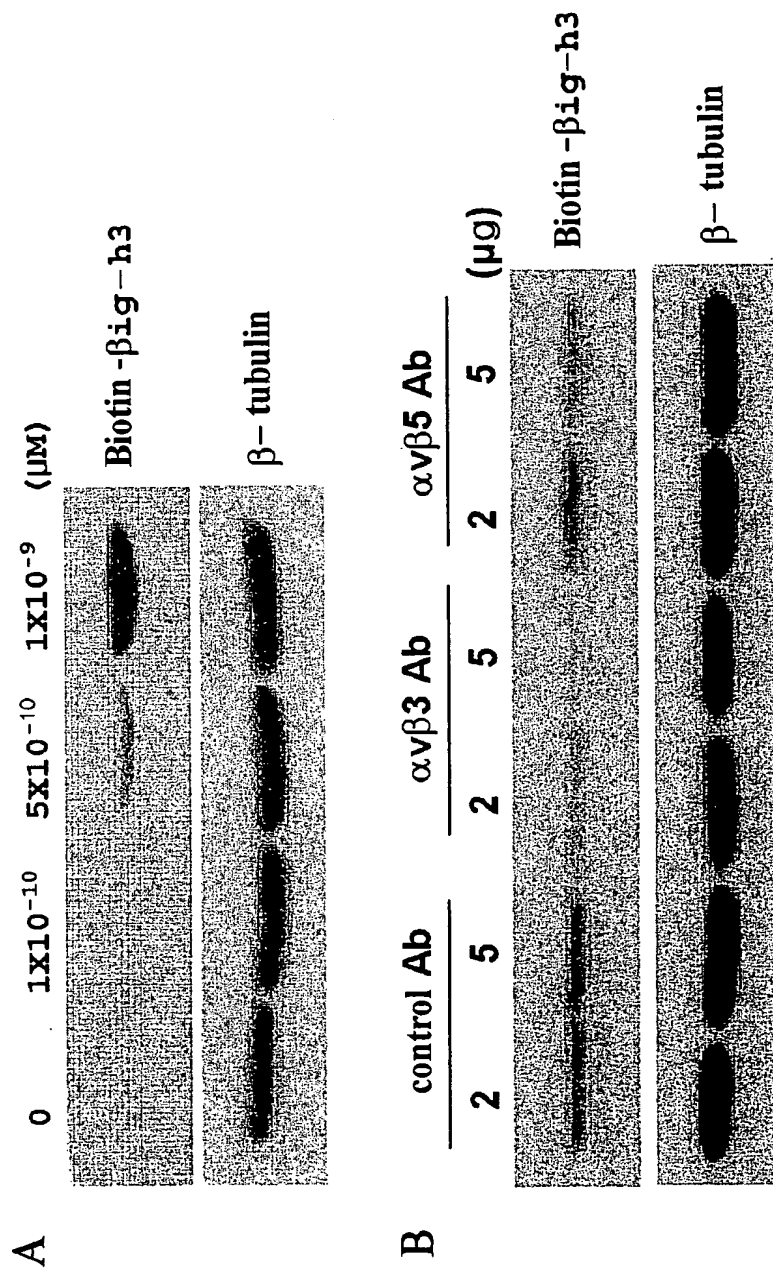
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FIG. 3c



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FIG. 3d



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FIG. 4a

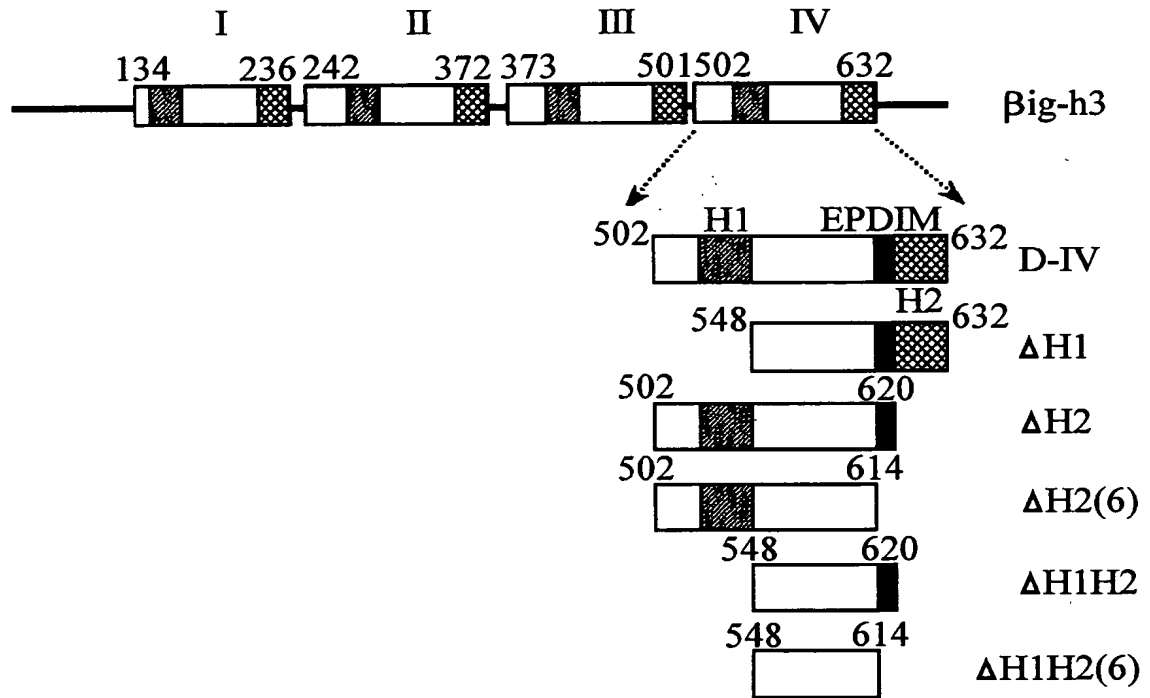


Figure 1: Schematic diagram and bar graph of the D-IV protein structure and its interaction with BSA.

Schematic Diagram (Left): The D-IV protein is shown as a linear sequence of amino acids from 134 to 632. It is divided into four domains: I (134-236), II (242-372), III (373-502), and IV (502-632). Domain I contains a hatched box. Domain II contains a hatched box and a solid black box. Domain III contains a hatched box and a solid black box. Domain IV contains a hatched box and a solid black box. The protein is labeled as β ig-h3, D-IV, and Δ H1H2(6). The H1 and H2 regions are indicated by arrows pointing to the solid black boxes in domains III and IV, respectively. The H1 region is labeled 502 and the H2 region is labeled 632. The H1 and H2 regions are also labeled 548 and 614, respectively.

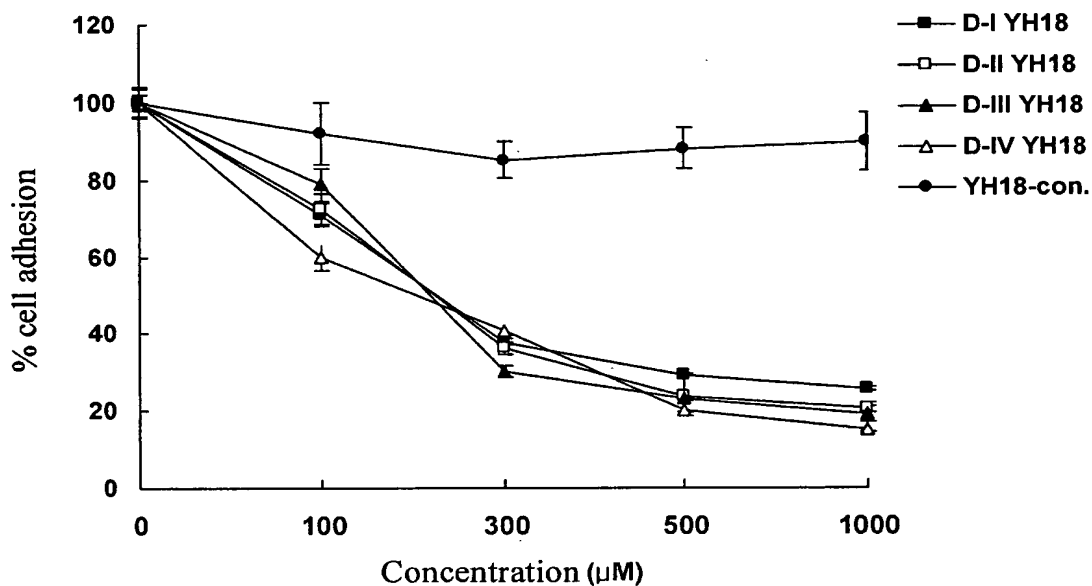
Bar Graph (Right): The bar graph shows the absorbance at 405 nm for various protein samples. The y-axis is labeled "Absorbance at 405nm" and ranges from 0.00 to 0.90. The x-axis lists the samples: BSA, D-IV, H1H2(6), AA, L, R, LYHR, LAA, and AAR. The absorbance values are approximately: BSA (0.05), D-IV (0.75), H1H2(6) (0.72), AA (0.70), L (0.70), R (0.70), LYHR (0.38), LAA (0.18), and AAR (0.35). Error bars are shown for each sample.

Sample	Absorbance at 405nm
BSA	0.05
D-IV	0.75
H1H2(6)	0.72
AA	0.70
L	0.70
R	0.70
LYHR	0.38
LAA	0.18
AAR	0.35

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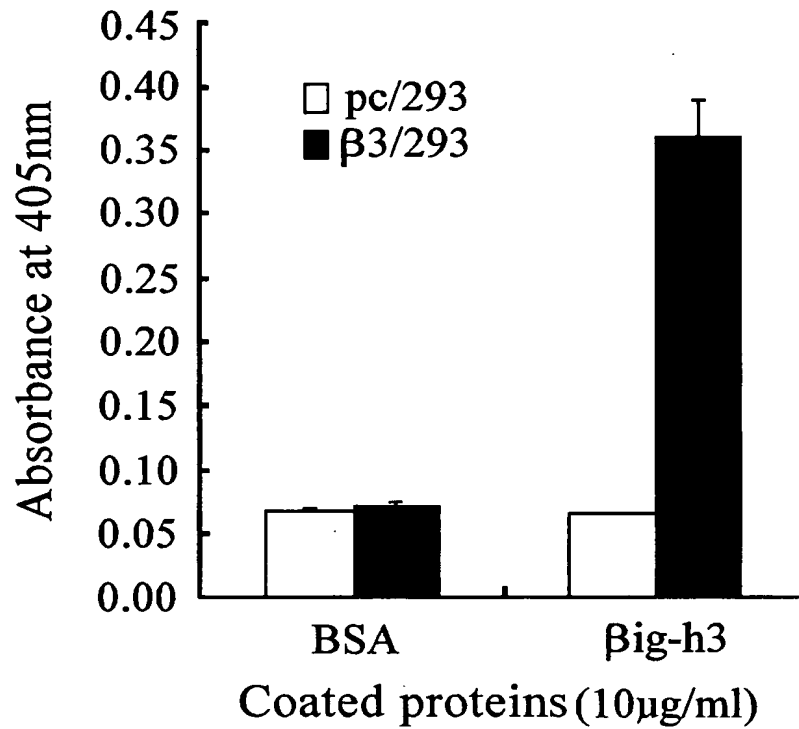
FIG. 5

D-I	YH18	165	IELLNALRYHMGRRVLT	182
D-II	YH18	301	EALRDLLNNHILKSAMCA	318
D-III	YH18	442	DQLASKYLYHGQTLETLG	459
D-IV	YH18	563	KELANILKYHIGDEILVS	580
YH18-con			KELANIHGKLYDEILVS	



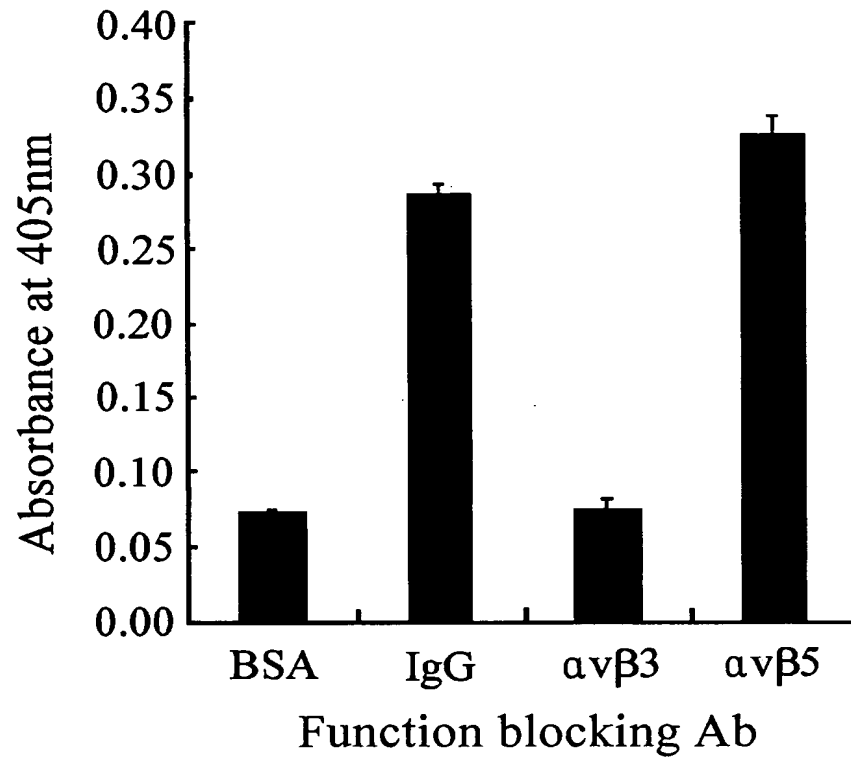
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FIG. 6a



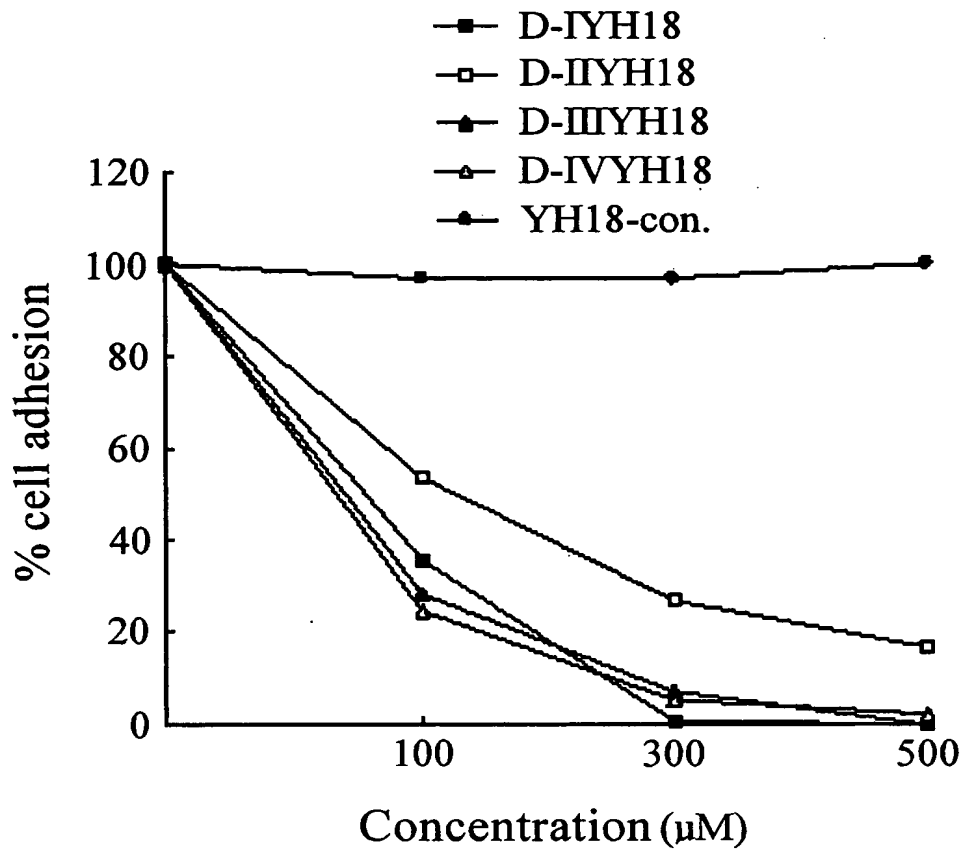
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FIG. 6b



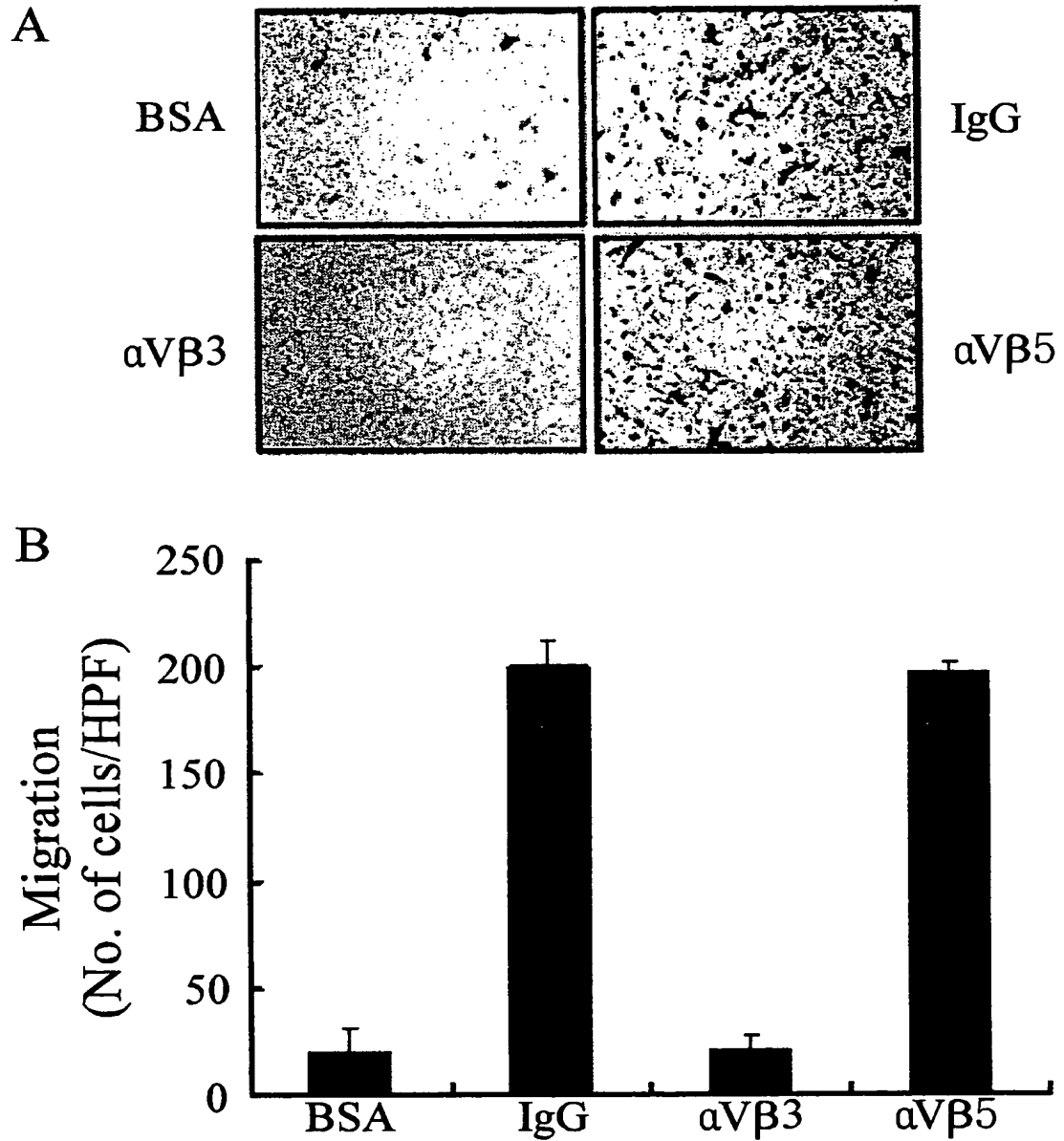
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FIG. 6c



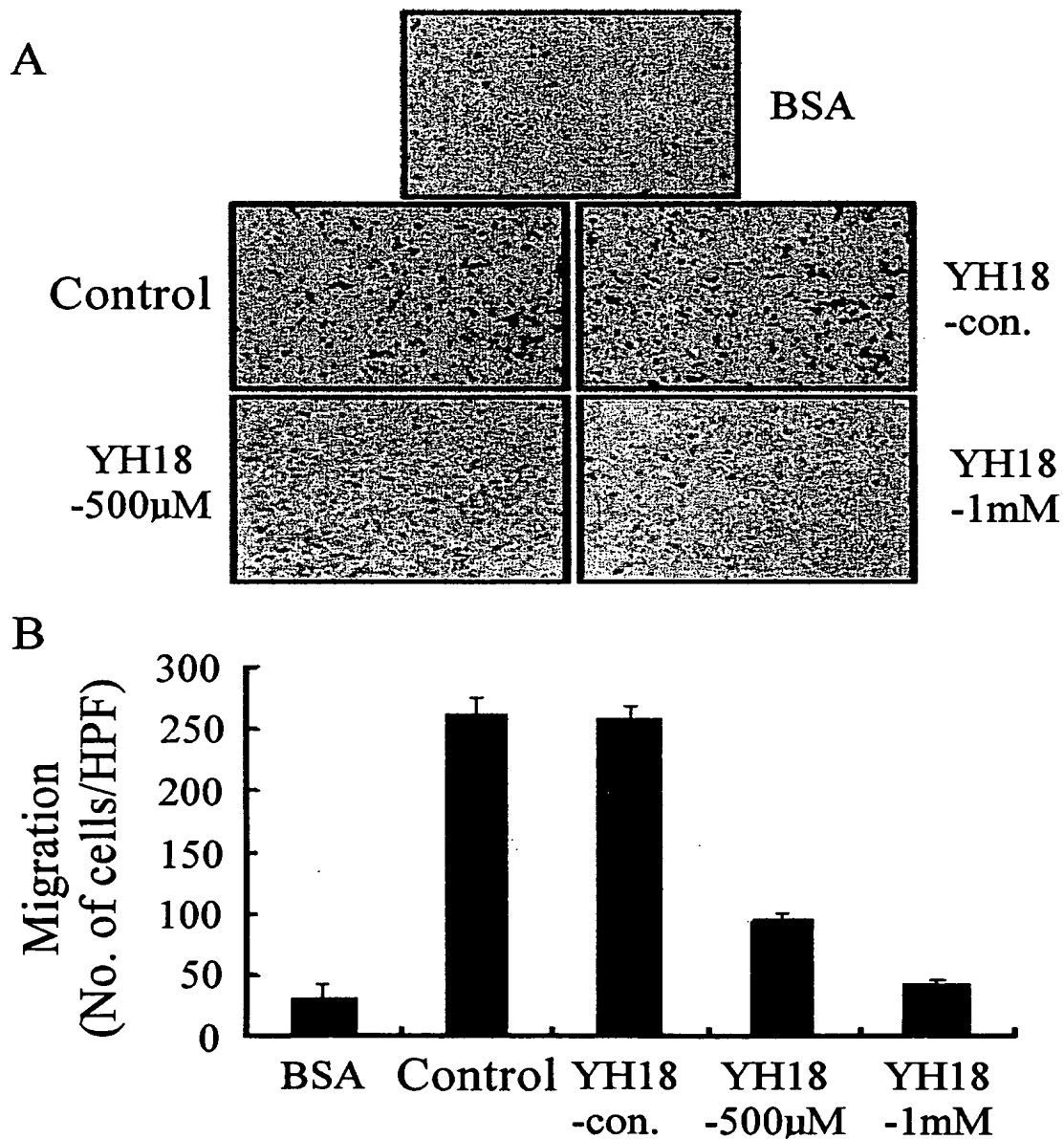
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FIG. 7a



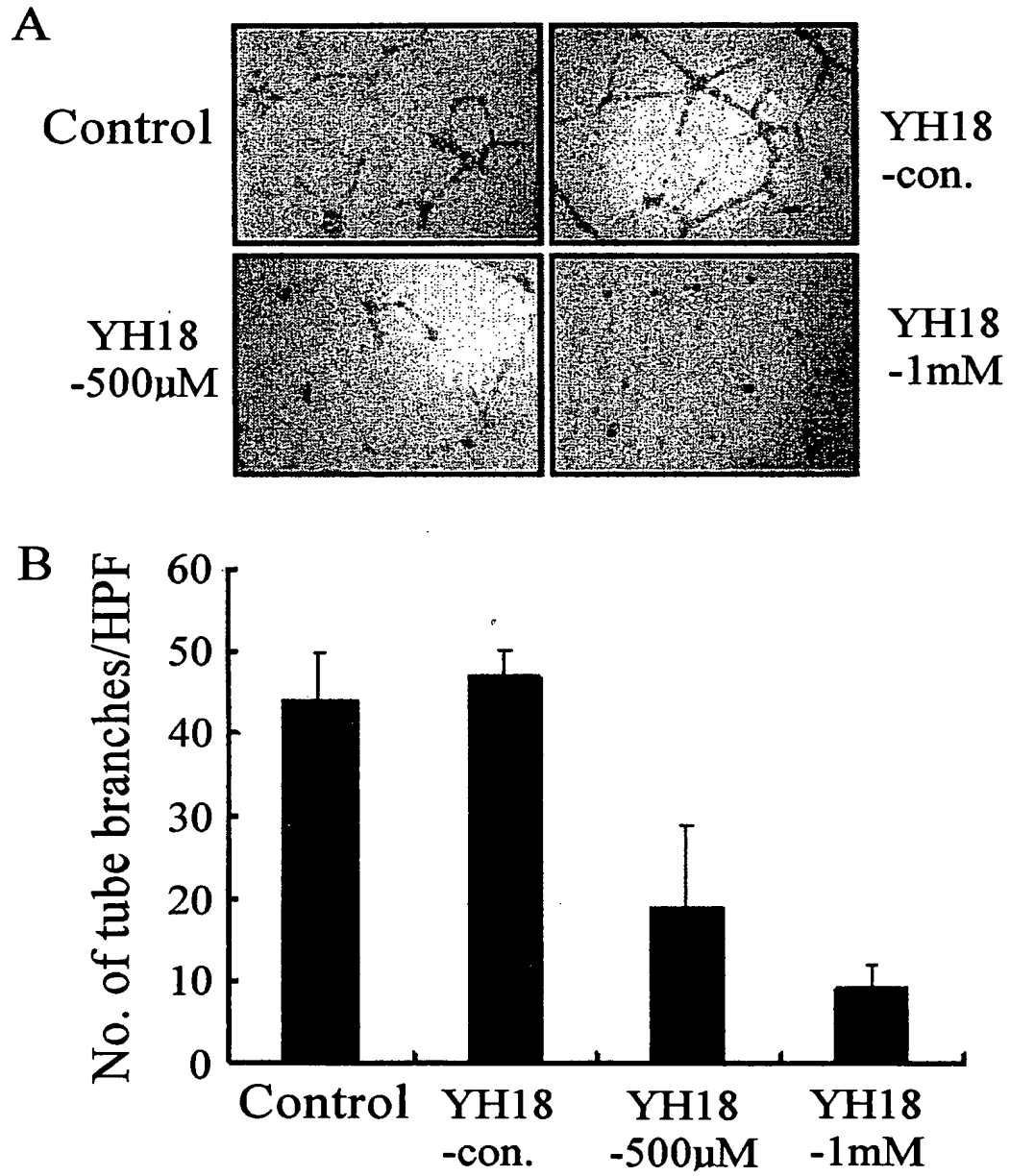
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FIG. 7b



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FIG. 8a



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FIG. 8b

